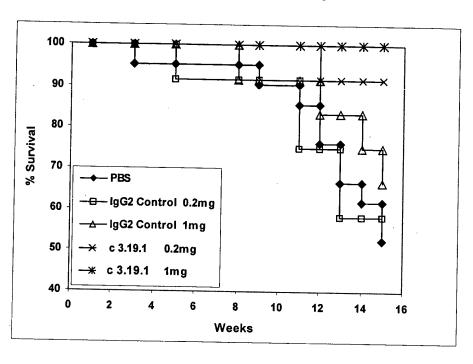


FIGURE 5



ANTI-MUC18 ANTIBODY C3.19.1

Nucleotide Sequence of heavy chain variable region

5'-

Amino Acid Sequence of Heavy Chain Variable Region

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYNPSLKSR VTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVSS (SEQ ID NO: 1)

Nucleotide Sequence of light chain variable region

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCC
TGCAGGTCTAGTCAGAGCCTCCTGCGTAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAG
CCAGGACAGTCTCCACATCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGG
TTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAGCTCAACAAAGTCCGATCACCTTCGGCCAAGGGACACGACTGGAG
ATTAAAC 3' (SEQ ID NO: 4)

Amino Acid Sequence of Light Chain Variable Region

DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRASGVPDR FSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK (SEQ ID NO: 2) Appl. No.: Not Assigned Atty Docket: ABGENIX.030C1

FIGURE 7

ANTI-MUC18 ANTIBODY C6.11.13

Nucleotide Sequence of heavy chain variable region

5'CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGCAGTGGTACTTACCACTGGAGCTGGATCCGCCAGCACCCAGGG
AAGGGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAG
AGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACT
GCCGCGGACACGGCCGTGTATTACTGTGCGAGAGGGGGAGATGGCTACAAGTACTGGGGCCAGGGA
ACCCTGGTCACCGTCTCCTCAG-3' (SEQ ID NO: 7)

Amino Acid Sequence of Heavy Chain Variable Region
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKYWGQGTLVTVSS (SEQ ID NO: 5)

Nucleotide Sequence of light chain variable region

Amino Acid Sequence of Light Chain Variable Region EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK (SEQ ID NO: 6)

ANTI-MUC18 ANTIBODY C3.10

Nucleotide Sequence of heavy chain variable region

- 1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC
- 61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT GGAGCTGGAT CCGGCAGCCC
- 121 CCAGGGAAGG GACTGGAGTG GATTGGCTAT ATCTATTACA CTTGGACCAC CAACTACAAC
- 181 CCCTCCCTCA AGAGTCGCGT CACCATATCA GTGGACACGT CCAAGAACCA GTTCTCCCTG
- 241 AGGCTGAGCT CTGTGACCGC TGCGGACACG GCCCTTTATT ACTGTGCGAG AGATCAGGGG
- 301 CAGTGGTTAC TACCCGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CACCGTCTCT
- 361 TCAG (SEQ ID NO: 11)

Amino Acid Sequence of Heavy Chain Variable Region

- 1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY IYYTWTTNYN
- 61 PSLKSRVTIS VDTSKNQFSL RLSSVTAADT ALYYCARDQG QWLLPDAFDI WGQGTMVTVS
- 121 S (SEQ ID NO: 9)

Nucleotide Sequence of light chain variable region

- 1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
- 61 ATCACTTGCC GGGCAAGTCA GAGCATTAGC AACTATTTAA ATTGGTATCA GCAGAAACCA
- 121 GGAAAAGCCC CTAAGCTCCT GATCTATGGT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
- 181 AGGTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
- 241 GAAGATTTTG CAACCTACTA CTGTCGACAG AGTTACAGTA CCCCTCCGGA GTGCAGTTTT
- 301 GGCCAGGGGA CCAAGCTGGA GATCAAAC (SEQ ID NO: 12)

- 1 DIQMTQSPSS LSASVGDRVT ITCRASQSIS NYLNWYQQKP GKAPKLLIYG ASSLQSGVPS
- 61 RFSGSGSGTD FTLTISSLQP EDFATYYCRQ SYSTPPECSF GQGTKLEIK (SEQ ID NO:
- 10)

ANTI-MUC18 ANTIBODY C3.22

Nucleotide Sequence of heavy chain variable region

1	CAGGTGCAGC	TGCAGGAGTC	GGGCCCAGGA	CTGGTGAAGC	CTTCACAGAC	CCTGTCCCTC
61	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGC	AGTGGTGGTT	ACTACTGGAC	TTGGATCCGC
121	CAGCACCCAG	GGAAGGGCCT	GGAGTGGATT	GGGTTCATCT	ATTACAGTGG	GAGCACCTAC
181	TACAACCCGT	CCCTCAAGAG	TCGAGTTACC	ATATCAGTAG	ACACGTCTAA	GAACCAGTTC
241	TCCCTGAAGC	TGAGCTCTGT	GACTGCCGCG	GACACGGCCG	TGTATTACTG	TGCGAGAGAG
301	GGAGATGGCT	TTGACTACTG	GGGCCAGGGA	ACCCTGGTCA	CCGTCTCCTC	AG (SEQ ID
NO:	15)					

Amino Acid Sequence of Heavy Chain Variable Region

1 QVQLQESGPG LVKPSQTLSL TCTVSGGSIS SGGYYWTWIR QHPGKGLEWI GFIYYSGSTY 61 YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAVYYCARE GDGFDYWGQG TLVTVSS (SEQ ID NO: 13)

Nucleotide Sequence of light chain variable region

1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC 61 ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG GCTGGTATCA GCAGAAACCA 121 GGGAAAGCCC CTAAGCGCCT GATCTATGCT GCATCCAGTT TGCAAAGTGG GGTCCCATCA 181 AGGTTCAGCG GCAGTGGATC TGGGACAGAA TTCACTCTCA CAATCAGCAG CCTGCAGCCT 241 GAAGATTTTG CAACTTATTA CTGTCTACAG CATAATAGTT ACCCGCTCAC TTTCGGCGGA 301 GGGACCAAGG TGGAGATCAA AC (SEQ ID NO: 16)

- 1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS
- 61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPLTFGG GTKVEIK (SEQ ID NO: 14)

Appl. No.: Not Assigned Atty Docket: ABGENIX.030C1

FIGURE 10

ANTI-MUC18 ANTIBODY C3.27

Nucleotide Sequence of heavy chain variable region

1	CAGGTGCAGC	TGCAGGAGTC	GGGCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	CCTGTCCCTC
61	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGT	AGTTACTACT	GGAGCTGGAT	CCGGCAGCCC
121	CCAGGGAAGG	GACTGGAGTG	GATTGGCTAT	ATCTATTACA	CTTGGACCTC	CAACTACAAC
181	CCCTCCCTCA	AGAGTCGCGT	CACCATATCA	GTGGACACGT	CCAAGAACCA	GTTCTCCCTG
241	AGGCTGAGTT	CTGTGACCGC	TGCGGACACG	GCCGTTTACT	ACTGTGCGAG	AGATCAGGGG
301	CAGTGGTTAC	TACCCGATGC	TTTTGATATC	TGGGGCCAAG	GGACAATGGT	CACCGTCTCT
361	TCAG (SEQ]	[D NO: 19)				

Amino Acid Sequence of Heavy Chain Variable Region

1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY IYYTWTSNYN 61 PSLKSRVTIS VDTSKNQFSL RLSSVTAADT AVYYCARDQG QWLLPDAFDI WGQGTMVTVS 121 S (SEQ ID NO: 17)

Nucleotide Sequence of light chain variable region

1	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	CAGAGTCACC
61	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AATGATTTAG	GCTGGTATCA	GCAGAAACCA
121	GGGAAAGCCC	CTAAGCGCCT	GATCTATGCT	GCATCCAGTT	TGCAAAGTGG	GGTCCCATCA
181	AGGTTCAGCG	GCAGTGGATC	TGGGACAGAG	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT
241	GAAGATTTTG	CAACTTATTA	CTGTCTACAG	CATAATAGTT	ACCCGTGGAC	GTTCGGCCAA
301	GGGACCAAGG	TGGAAATCAA	AC (SEQ ID	NO: 20)		4

Amino Acid Sequence of Light Chain Variable Region

1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS 61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPWTFGQ GTKVEIK (SEQ ID NO: 18) Appl. No.: Not Assigned Atty Docket: ABGENIX.030C1

FIGURE 11

ANTI-MUC18 ANTIBODY C3.45

Nucleotide Sequence of heavy chain variable region

1	CAGGTTCAGC	TGGTGCAGTC	GGGAGCTGAG	GTGAAGAAGC	CTGGGGCCTC	AGTGAAGGTC
61	TCCTGCAAGG	CTTCTGGTTA	CACCTTTTTT	AGCTATGGTT	TCAGCTGGGT	GCGACAGGCC
121	CCTGGACAAG	GGCTTGAGTG	GCTGGGATGG	ATCAGCGCTT	ACAATGGTAA	CACAAACTAT
181	GCACAGAAGC	TCCAGGGCAG	AGTCACCATG	ACCACAGACA	CTTCCACGAG	CACAGCCTAC
241	ATGGAGCTGA	GGAGCCTGAG	ATCTGACGAC	ACGGCCGTGT	ATTACTGTGC	GAGAGAAACT
301	AAGGTTCGGG	GAGTCCACTA	CTACGGTATG	GACGTCTGGG	GCCAAGGGAC	CACGGTCACC
361	GTCTCCTCAG	(SEQ ID NO:	: 23)			

Amino Acid Sequence of Heavy Chain Variable Region

1 QVQLVQSGAE VKKPGASVKV SCKASGYTFF SYGFSWVRQA PGQGLEWLGW ISAYNGNTNY 61 AQKLQGRVTM TTDTSTSTAY MELRSLRSDD TAVYYCARET KVRGVHYYGM DVWGQGTTVT 121 VSS (SEQ ID NO: 21)

Nucleotide Sequence of light chain variable region

1 DIVMTQSPDS LAVSLGERAT IICKSSQSIL YSSNNKNYLG WYQQKPGQPP KLLIYWASTR 61 ESGVPARFSG SGSGTDFTLT INSLQAEDVA VYYCQQYYST PRSFGQGTMV EIK (SEQ ID NO: 24)

1	GACATCGTGA	TGACCCAGTC	TCCAGACTCC	CTGGCTGTGT	CTCTGGGCGA	GAGGGCCACC
61	ATCATCTGCA	AGTCCAGCCA	GAGTATTTTA	TACAGCTCCA	ACAATAAGAA	CTACTTAGGT
121	TGGTACCAGC	AGAAACCAGG	ACAGCCTCCT	AAGCTGCTCA	TTTACTGGGC	ATCTACCCGG
181	GAATCCGGGG	TCCCTGCCCG	ATTCAGTGGC	AGCGGGTCTG	GGACAGATTT	CACTCTCACC
241	ATCAACAGCC	TGCAGGCTGA	AGATGTGGCA	GTTTATTACT	GTCAGCAATA	TTATAGTACT
301	CCTCGGTCGT	TCGGCCAAGG	GACCATGGTG	GAAATCAAAC	(SEQ ID NO:	: 22)

ANTI-MUC18 ANTIBODY C3.65

Nucleotide Sequence of heavy chain variable region

1	CAGGTGCAGC	TGCAGGAGTC	GGGCCCAGGA	CTGGTGAAGC	CTTCACAGAC	CCTGTCCCTC
61	ACCTGCACTG	TCTCTGGTGG	CTCCATCAAC	AGTGGTGGTT	GCTACTGGAG	CTGGATCCGC
121	CAGCACCCAG	GGAAGGGCCT	GGAGTGGATT	GGGTACATCT	ATTCCAGTGG	GAGCACCTAC
181	TACAACCCGT	CCCTCAAGAG	TCGAATTACC	TTATCAGTAG	ACACGTCTAA	GAACCAGTTC
241	TCCCTGAAGC	TGAACTCTAT	GACTGCCGCG	GACACGGCCG	TGTATTACTG	TGCGAGAGAT
301	CGGGAAACAG	CTGGTTTTGA	CTACTGGGGC	CAGGGAACCC	TGGTCACCGT	CTCCTCAG (SEQ
ID N	NO: 27)					

Amino Acid Sequence of Heavy Chain Variable Region

1 QVQLQESGPG LVKPSQTLSL TCTVSGGSIN SGGCYWSWIR QHPGKGLEWI GYIYSSGSTY 61 YNPSLKSRIT LSVDTSKNQF SLKLNSMTAA DTAVYYCARD RETAGFDYWG QGTLVTVSS (SEQ ID NO: 25)

Nucleotide Sequence of light chain variable region

1	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	CAGAGTCACC
61	ATCACTTGCC	AGGCGAGTCA	GGACATTAAC	AACTATTTAA	ATTGGTATCA	GCAGAAACCA
121	GGGAAAGCCC	CTAAGCTCCT	GATCTACGAT	GCATCCAATT	TGGAAACAGG	GGTCCCATCA
181	AGGTTCAGTG	GAAGTGGATC	TGGGACAGAT	TTTACTTTCA	CCATCAGCGG	CCTGCAGCCT
241	GAGGATATTG	CAACATATTA	CTGTCAACAG	TATGATACTC	TCCCTCTCAC	TTTCGGCGGC
301	GGGACCAAGG	TGGAGATCAA	AC (SEQ ID	NO: 28)		

- 1 DIQMTQSPSS LSASVGDRVT ITCQASQDIN NYLNWYQQKP GKAPKLLIYD ASNLETGVPS
- 61 RFSGSGSGTD FTFTISGLQP EDIATYYCQQ YDTLPLTFGG GTKVEIK (SEQ ID NO: 26)

Appl. No.: Not Assigned Atty Docket: ABGENIX.030C1

FIGURE 13

ANTI-MUC18 ANTIBODY C6.1

Nucleotide Sequence of heavy chain variable region

1	CAGGTGCAGC	TGGTGGAGTC	GGGGGGAGGC	GTGGTCCAGC	CTGGGAGGTC	CCTGAGACTC
C1	macmamaa a	COMOMOCAMM	OR COMMOROM	3 COM 3 M COO 3	maar amaaam	000007000

- 61 TCCTGTGCAG CCTCTGGATT CACCTTCAGT AGCTATGCCA TGCACTGGGT CCGCCAGGCT
- 121 CCAGGCAAGG GGCTGGAGTG GGTGGCAGTT ATATCATATG ATGGAAGTAA TAAATACTAT
- 181 GCAGACTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT
- 241 CTGCAAATGA ACAGCCTGAG AGCTGAGGAC ACGGCTGTGT ATTACTGTGC GAGATCGATT
- 301 TTTGGAGTGG TTATCGACTA CGGTATGGAC GTCTGGGGCC AAGGGACCAC GGTCACCGTC
- 361 TCCTCAG (SEQ ID NO: 31)

Amino Acid Sequence of Heavy Chain Variable Region

- 1 QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYAMHWVRQA PGKGLEWVAV ISYDGSNKYY
- 61 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARSI FGVVIDYGMD VWGQGTTVTV
- 121 SS (SEQ ID NO: 29)

Nucleotide Sequence of light chain variable region

- 1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
- 61 ATCACTTGCC GGGCGAGTCA GGGCATTAGA AATTATTTAG CCTGGTATCA GCAGAATCCA
- 121 GGGAAAGTTC CTAAGCTCCT GATCTATGGT GCATCCACTT TGCAATCAGG GGTCCCATCT
- 181 CGGTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG CCTGCAGCCT
- 241 GAAGATGTTG CAACTTATTA CTGTCAAAAG TTTAGCAGTC CCCCATTCAC TTTCGGCCCT
- 301 GGGACCAAAG TGGATATCAG TC (SEQ ID NO: 32)

- 1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NYLAWYQQNP GKVPKLLIYG ASTLQSGVPS
- 61 RFSGSGSGTD FTLTISSLQP EDVATYYCQK FSSPPFTFGP GTKVDIS (SEQ ID NO: 30)

ANTI-MUC18 ANTIBODY C6.9

Nucleotide Sequence of heavy chain variable region

1	CAGGTGCAGC	TGGAGCAGTC	GGGGCCAGGA	CTGGTGAAGC	CTTCAGAGAC	CCTGTCCCTC	
61	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGC	AGTGGTACTT	ACCACTGGAG	CTGGATCCGC	
121	CAGCACCCAG	GGAGGGGCCT	GGAGTGGATT	GGATACATCT	ATTACAGTGG	GAGCACCTAC	
181	CACAACCCGT	CCCTCAAGAG	TCGAATTACC	ATATCAGTAG	ACACGTCTAA	GAACCAGTTC	
241	TCCCTGAAGC	TGAGCTCTGT	GACGGCCGCG	GACACGGCCG	TGTATTACTG	TGCGAGAGGG	
301	GGAGATGGCT	ACAGATACTG	GGGCCAGGG	A ACCCTGGTC	A CCGTCTCC	rc ag (seq	ΙD
NO:	35)						

Amino Acid Sequence of Heavy Chain Variable Region

1 QVQLEQSGPG LVKPSETLSL TCTVSGGSIS SGTYHWSWIR QHPGRGLEWI GYIYYSGSTY 61 HNPSLKSRIT ISVDTSKNQF SLKLSSVTAA DTAVYYCARG GDGYRYWGQG TLVTVSS (SEQ ID NO: 33)

Nucleotide Sequence of light chain variable region

1 GAAATAGTGA TGACGCAGTC TCCAGCCACC CTGTCTGTGT CTCCAGGGGA AAGAGCCACC 61 CTCTCCTGCA GGGCCAGTCA GAGTATTAGC AACAACTTCG CCTGGTACCA GCAGAAACCT 121 GGCCAGGCTC CCAGGCTCCT CATCTTTGGT GCATCCACCA GGGCCACTGG TATCCCAGCC 181 AGGTTCAGTG GCAGTGGGTC TGGGACAGAA TTCACTCTCA CCATCAGCAG CCTACAGTCT 241 GAAGATTTTG CAGTTTATTA CTGTCAGCAG TATAATAACT GGCCTCGGAC GTTCGGCCAA 301 GGGACCAAGG TGGAAATCAA AC (SEQ ID NO: 36)

- 1 EIVMTQSPAT LSVSPGERAT LSCRASQSIS NNFAWYQQKP GQAPRLLIFG ASTRATGIPA
- 61 RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YNNWPRTFGQ GTKVEIK (SEQ ID NO: 34)

ANTI-MUC18 ANTIBODY C6.2

Nucleotide Sequence of heavy chain variable region

- 1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CCTCGGAGAC CCTGTCCCTC
- 61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT ACTTACTACT GGAGTTGGAT CCGGCAGCCC
- 121 CCAGGGAAGG GACTGGAGTG GATTGGATAC ATCTATTACA CTGGGAACAC CTACTACAAC
- 181 CCCTCCCTCA AGAGTCGAGT CACCGTTTCA GTTGACACGT CCAAGAACCA GTTCTCCCTG
- 241 AAGCTGAACT CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGCGAG AGATCCAGGC
- 301 CAGTGGCTGG TCCCTGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CTCCGTCTCT
- 361 TCAG (SEQ ID NO: 39)

Amino Acid Sequence of Heavy Chain Variable Region

- 1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS TYYWSWIRQP PGKGLEWIGY IYYTGNTYYN
- 61 PSLKSRVTVS VDTSKNQFSL KLNSVTAADT AVYYCARDPG QWLVPDAFDI WGQGTMVSVS
- 121 S (SEO ID NO: 37)

Nucleotide Sequence of light chain variable region

- 1 GATATTGTGA TGACTCAGTC TCCACTCTCC CTGCCCGTCA TTCCTGGAGA GCCGGCCTCC
- 61 ATCTCCTGCA GGTCTAGTCA GAGCCTCCTG CAGAGTAATG GAAACAACTA TTTGGATTGG
- 121 TACCTGCAGA AGCCAGGGCA GTCTCCACAG CTCCTGATCT ATTTGGGTTC TAATCGGGCC
- 181 TCCGGGGTCC CTGACAGGTT CAGTGGCAGT GGATCAGGCA CAGATTTTAC ACTGAAAATC
- 241 AGCAGAGTGG AGGCTGACGA TGTTGGGATT TATTACTGCA TGCAAGCTCT CCAAATTCCT
- 301 CTCACTTTCG GCGGAGGGAC CAAGGTGGAG ATCAAAC (SEQ ID NO: 40)

- 1 DIVMTQSPLS LPVIPGEPAS ISCRSSQSLL QSNGNNYLDW YLQKPGQSPQ LLIYLGSNRA
- 61 SGVPDRFSGS GSGTDFTLKI SRVEADDVGI YYCMQALQIP LTFGGGTKVE IK (SEQ ID NO: 38)

				, : 				- Section 1
	(1)	1	,10		20	30	40	53
A15-3.10 HC	(1)	QVQ:	LQESGPGL	VKPSETLS	ILTCTVSGG	Sissyyb	JUWI ROPPGKGI	EWIGYIYY
VH4-59	(1)						JEWIRQPPGKGI	
Consensus	(1) ——	QVQ	LQESGPGL	VKPSETLS	BLTCTVSGG	SISSYYV	JSWIRQPPGKGI	EWIGYIYY — Section 2
	(54)	54	60	70	80)	90	106
A15-3.10 HC		DW D	TNYNPSLK	SRVTTSVI	текиорет	RTSSVT!	ADTATYYCARI	OGOMITED
VH4-59		9GS	TNYNPSLK	SRVTTSVI	лекиореі.	KT.SSV#2	ADTAVYYCAR-	
Consensus	(54)	104 Taris					ADTALYYCAR	
	(5.,							- Section 3
1	(107)	107		121				000000
A15-3.10 HC	107)	AFD	IWGQGTMV	TVSS				
VH4-59	(98)							
Consensus								

positives: 79,3% lidentity: 76,0%

١

								Section 1
	(1)	1	10		20	30	40	53
A15-3.10_LC	(1)	DIOM	rospasi	JASVÉDR	VTITCE	ABQBISN	YLNWYOORPGR	APKLLTY G ASS
02	(1)	DIOM	rogpasj	RABUGD'R	ur erci	ASQSISS	YINWYOOKEGK	aekluly a ass
Consensus	(1)	DIQM	rQapaa1	SASVGDR	VTITCE	RIEDEA	YLNWYQQKPGR	APKLLIYAASS
								Section 2
	(54)	54	60	70		80	90	106
A15-3.10_LC	(54)	LOSG	ve srps(SGEGTDF.	TLTLS	ILOPEDFA	TYYCROSYSTE	PECSFGQGTKL
02	(54)	LOSG	JPSRF3(Sesetdf	TLTIS	idopedfa	TXXCODSYSTE	
Consensus	(54)	LQSG	VPSRFS	SESSTDF	TLTISS	LQPEDFA	TYYC QSYSTE	•
								Section 3
	(107)	107						
A15-3.10 LC	(107)	EIK						
02	(96)							
Consensus	(107)							

				FIGUR	10		
	<i>a</i> v 1		10		 30	40	Section 1
445 0 20 110	(1)	THE RESERVE OF THE PARTY.				70	421000000000000000000000000000000000000
A15-3.22 HC	(1)		En at GUAL			CT THIS HILK LE	PGKGDBWIGE
VH4-31							PEKETRWICX
Consensus	(1)	GAGTG	esgpglvk	PSQTLSLTC	TVSGGSISS	GYYWSWIRQH	PGKGLEWIGF
							Section 2
	(54)	54	60	70	80	90	10
A15-3.22 HC	(54)	vyscá	TVVNESTA	AR OPTAVET	GKNORSTIKE.	VVATGĀTVE	YCAREGDGED
VH4-31	(5A)	vvaca	myzkipat v	apim reurn	akn batki.	SUTAADTAVY	VP30
						SVTAADTAVY	
Consensus	(34)	11363	TIINPSLK	SKVIISVDI	SVMCLSTVTG	SVIAADIAVI	
							Section 3
	(107)	107	117				
A15-3.22 HC	(107)	WGQGT	LVTVSS				
VH4-31					*		•
Consensus							
Consensus	(107)						

positives: 84:6% identity: 82.9%;

		<u> </u>					Section 1
	(1)	1	,10	20	30	40	53
A15-3.22 LC	(1)	DIOM	rospaslis	IABVGDRVTIT	CRASOGIRNI	LGWYOOKPGE	BEAKTIJANGA
A30	(1)	DIOM	IOSPSSI:	BASVEDRUTIT	CRASOGIRNE	LGWYQOKPGR	APKRITYAARG
Consensus	(1)	DIQM	rqspssls	BASVGDRVTIT	CRASQGIRND	LGWYQQKPGF	APRRLIYAASS
							Section 2
	(54)	Contract Con	60	<u>7</u> 0	80	90	106
A15-3.22_LC	(54)	roae	VP BRF SGS	G9GTEFTLTI	SSLOPEDFAT	YYCLOHNSYE	LTFGGGTKVEI
A30	(54)	LOSG	VP SRF 8GS	GBGTEFTLTI	SSLOPEDFAT	YYCLOHNSYE	
Consensus	(54)	rose.	VPSRFSGS	GSGTEFTLTI	SSLQPEDFAT	YYCLQHNSYE	i
						· · · · · · · · · · · · · · · · · · ·	Section 3
	(107)						
A15-3.22_LC	·	K					
A30	(96)	-					
Consensus	(107)						
							,

positives: 88.8% | jidentity: 88.8%

USE OF ANTIBODIES AGAINST THE MUC18 ANTIGEN Bar-Eli et al.

Appl. No.: Not Assigned Atty Docket: ABGENIX.030C1

FIGURE 20

— Section 1	_ 						
53	40	30	20	.10	1	(1)	
EWIGYIYY	SWIRQPPGKG	GGSISSYY	TLSTTCT!	ESGPGLVKPS	QVQLQE:	(1)	A15-3.27 HC
EWIGYIY:	BWIRQPPGKG:	GGSISSYY	STEBLICTY	ESGPGLVKP S	QVQLQE:	(1)	VH4-59
EWIGYIYY — Section 2	SWIRQPPGKG:	GGSISSYY	TLSLTCT	ESGPGLVKPS	OVOLOE	(1)	Consensus
108	90	80	70	60	54 8	(54)	
GGGMLTAI	ADTAVYYCAR	SLRLSSVT	Landaskn(YNP SLKSRVI	TWESWY		A15-3.27 HC
	ADTAVYYCAR	SLKLSSVT	CSVDTSKNO	YNPSLKSRVI	SGETNY	(54)	VH4-59
	ADTAVYYCAR					(54)	Consensus
Section 3						<u>`</u>	
`				121	107	(107)	
			-	GQGTMVTVSS	AFDIWG	(107)	A15-3.27 HC
						`(98)	∨H4-59
						MOZÍ	Consensus

positives: 79.3% identity: 76.0%

				·			Section 1
	(1)	1	,10	20	30	40	53
A15-3.27 LC	(1)	DICHT	OSPESTS	AHVGDR VTI	TCRASOGIRNI	TGWYQQKBGK	NEKRUTYAA 39
A30	(1)	DIOMI	озвазиз	ASVGDRVIL	<u>TCRABOGLÁNI</u>	PCMAGOKECK	MERRITA AAGS
Consensus	(1)	DIQMI	Gabaara	ASVGDRVTI	TCRASQGIRNI	LGWYQQKPGK	REKAYIJANGS
							Section 2
	(54)		60	/ 70	80	90	106
A15-3.27_LC	(54)	hosev	vesar sig	GBGTERTIT	ISSEQUEDFA!	yychohnsyei	WTFGQGTKVEI
A30	(54)	TOSG	/PBRF.CGS	GSGTEFTLT	ISSLOPEDPA!	CAACTOHNEAD	
Consensus	(54)	LQSGV	PSRFSGS	GSGTEFTLT	ISSLQPEDFAT	TYYCLQHNSYP	
							Section 3
((107)	107					
A15-3.27_LC	(107)	K					,
A30	(96)	-					
Consensus	(107)						

positives: 88.8%, dentity, 88.8%;

								- Section 1
	(1)	1	,10	21	3	30	40	53
A15-3.45 HC	(1)	OVOL	VQSGAEVI	KREGASVKV	SCKASGYTE	FSYGFSWVP	QAPGQGLI	ew i gwisa
VH1-18	(1)	OAOP	VOSGAEVE	(KPGABVKV	SCKASGYTE	TBYGISWVP	QAPGQGLI	EWMGWISA
Consensus	(1)	QVQL	VQSGAEVI	KPGASVKV	SCKASGYTE	Y SYG SWVR	QAPGQGLI	EWLGWISA Section 2
	(54)	54	60	70	80	90		106
A15-3.45_HC	(54)	YNGN	TNYAQKLO	GRVTMTTD	TSTSTAYME	LRSLRSDDT	AVYYCARI	ETKVRGVH
VH1-18	(54)	YNGN	TNYAQKLO	grvtm i td	TBTSTAYME	LRSLRSDDT	AVYYCAR-	
Consensus	(54)	YNGN	TNYAQKLO	GRVTMTTD	TSTSTAYME	LRSLRSDDT	AVYYCAR	
								Section 3
	(107)	107		123				
A15-3.45_HC	(107)	YYGM	DVWGQGTT	REVTVE				
VH1-18	(99)							
Consensus	(107)							
				positives: 78.0%	identity: 77.29			•

<u></u>	(1)	1	.10	20	30	40	——— Section 1 53
A15-3.45_LC	(1)	DIVM	rosedstā	VSLGERATI	rckasoa i ns	SSNNKNYL Š WY	OOKPGOPPRIT
B3	(1)	DIVM	<u>rqspdsla</u>	VBLGERATT	NCKSSOSVI	ZSSNNKNYLÄWY	OOKEGOPPKTIT
Consensus	(1)	DIVM	rdabdard.	VSLGERATI	CKSSQSIL	YSSNNKNYLAWY	QQKPGQPPKLL
							Section 2
	(54)	54	60	70	80	90	106
A15-3.45_LC	(54)	TYWAS	STRESGVE	ARFSGSGSG	POFTETINS	JOAED VAVYYCO	OYYSTERSEGO
B3	(54)	TYWAS	TRESGVE	DRESGSGS	PDFTLTISS	JQAEDVAVYYCQ	оууатр
Consensus						LQAEDVAVYYCQ	
							Section 3
	(107)	107	113				
A15-3.45_LC ((107)	GTMVE	BIK				
B 3 ((102)		- 				
Consensus ((107)						

positives: 86.7% Identity: 85,0%

,	(4)	1			20	30	40	Section 1
A15-3.65 HC	(1)	######################################			20			
	(1)						CYWSWIROHEG	
VH4-31	(1)	QV	OFOERCAGE	Pakesol	<u> Laplicir</u>	aecaraace	YYWSWIROHPO	KGLEWIGYI
Consensus	(1)	QV	Ordeache	Lake 2 di	LSTICIA	aeeai aee	YWSWIRQHPO	KGLEWIGYI
								Section 2
	(54)	54	60	70)	80	90	106
A15-3.65 HC	(54)		SGSTYYNP	arkarin	Тауртак	NOFSLKINS	MTAADTAVÝY	ARDRETAGE
VH4-31							VTAADTAVYY	
Consensus	(54)		SGSTYYNP				MTAADTAVYY	
CONSCISUS	(34)		DGSTIINE	PROKIT	TOADLOV	MOLDHUR S		Section 3
	(107)	107	(119				
A15-3.65 HC	(107)	DY	WGQGTLVT	VSS				
VH4-31								
Consensus	,		•					

positives: 79.8% identity: 77.3%

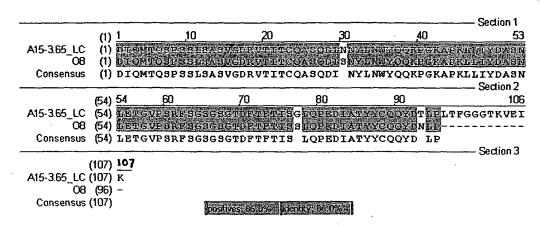


FIGURE 26

53	,40	30	. 20	,10	(1) 1	
YEIVAVN	MHWVRQAPGKGLI	SGFTFSSYA	GRSLRISCA	. VE 3GĞGVVQPG		A15-6.1 HC
YEIVAVN	MHWVRQAPGKGLI	SGFTFSSYG	SRSLRLSCA	LVESGGGVVQP	(1) QVQL	VH3-30
YZZIVAVW	MHWVRQAPGKGLE	SGFTFSSYA	GRSLRLSCA	LVESGGGVVQPG	(1) QVQL	Consensus
Section 2						
108	90	-80	70	60	54) 54	
	RAEDTAVYYCARS	TLYLOMNSI	TISRDNÍK	NKYYADSVKGRE	54) DGSN	A15-6.1 HC
	RAEDTAVYYCAR; RAEDTAVYYCAR-	Section and deposit of the experience of the contract of the c		14 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	22 / - W. W. W. W. W.	A15-6.1_HC VH3-30
	RAEDTAVYYCAR-	TLYLOMNSI	FIISRDNSF	vkyyad svkgrf	54) dgsn	_
IFGVVID	the second second the second s	TLYLOMNSI	FIISRDNSF	vkyyad svkgrf	54) dgsn	∨H3-30
	RAEDTAVYYCAR-	TLYLOMNSI	FIISRDNSF	YKYYAÖSVKGRY HASNVEDAYYN	54) dgsn	VH3-30 Consensus
IFGVVID	RAEDTAVYYCAR-	TLYLOMNSI	FTISRDNSF FTISRDNSF 22_	YKYYAÖSVKGRY HASNVEDAYYN	54) DGSN 54) DGSN 07) <u>107</u>	VH3-30 Consensus
IFGVVID	RAEDTAVYYCAR-	TLYLOMNSI	FTISRDNSF FTISRDNSF 22_	NKYYADSVKGRE NKYYADSVKGRE 1	54) DGSN 54) DGSN 07) <u>107</u>	VH3-30 Consensus (A15-6.1_HC (

positives: 80.3% identity: 79.5%

	(1)	1	11	D ·	20		 30	40	Section 1 54
A15-6.1 LC A20	(f) (f)	DIOM	rospas	LSASVGD	RVTITO	RASOGI	RNYLAWYC	ONEGRO	iekuerey gased jekulenyaasidi
Consensus	(1)								PKLLIYAASTL
	(55)	55	60	70		80	90		Section 2 107
A15-6.1_LC	(55)								FGPGTKVDIS
A20	(55)	oaev	PSRFAG	SESETDE	TLTIS	BLOPEDV	atyycor <u>3</u>	NBAB	
Consensus	(55)	QSGV:	PSRFSG	SGSGTDF	TLTISS	SLQPEDV.	ATYYCQKE	e a p	



FIGURE 28

							Section 1
	(1)	1		20	30	40	53
A15-6.12 HC	(1)	QVQLE	OSGPGL'	VKPSETLSL	CTVSGGSIS	GTYHWSWIROI	HPGRGLEWIGYI
VH4-31	(1)	QVQLC	DESGEGL	VKPSQTLSL	PCTV8GG8I3:	GGYYWBWIRO	HPGKGLEWIGYI
Consensus	(1)	QVQL	SGPGL	VKPS TLSL	CTVSGGSISS	G YHWSWIRQI	HPGKGLEWIGYI
							Section 2
	(54)	54	60	70	80	90	106
A15-6.12 HC	(54)	YYSGS	STYHNES	KSRTTISVI	такмогацкі	VATGAATVEE	YYCARGGDGYRY
VH4-31		YYSGS	TYYNPS	ckseVrisvi	TSKNOFSLKI	, BSVTAADTAV	YYCAR
Consensus	(54)	YYSGS	STYHNPS	LKSRITISVI	TSKNOFSLKI	VATGAATVEE	YYCAR
	(- ·/						Section 3
f	(107)	107	117				
A15-6.12 HC	. ,		LVTVSS	-			
VH4-31	• ,						
Consensus	• •						

positives: 81-2% Jidentify: 77.6%

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FIGURE 29

								- Section 1
	(1)	1	10		20	30	,4 0	53
12	(1)	EIVI	MTQSPATL	SVSPGERA	TISCRASOS	Jasnlawyo	ORPGOAPR	TEADYILL
A15-6.12_LC	(1)				TLECRASOS			
Consensus	(1)	EIV	TAGEOTH	SVSPGERA	TLSCRASQS	ОУWА И В	QKPGQAPR	LLIFGAST
								Section 2
	(54)	54	60	. 70	80			106
12	(54)				LTIBBLQBE			
A15-6.12_LC	(54)	TAR	SIPARFEG	SGBGTEFT:	Pata apo a e i	FAVYYCOO	YNNWPRTF	GQGTKVEI
Consensus	(54)	RAT	SIPARFSG	SGSGTEFT:	LTISSLQSE	PAVYYCQQ	YNNWP	
								Section 3
	(107)	107						
12	(96)	_						
A15-6.12_LC	(107)	K						
Consensus	(107)							
			. 6	Service Contract	and the second	76		

positives: 86,9% identity: 85,0%

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FIGURE 30

— Section 1								
53	40	30	20	<u> </u>		1	(1)	
WIGYIYY	SWİROPPEKEL	SBIBTYY	LSLTCTVS	LVKPSE	QESGP	QVQ	(1)	A15-6.2 HC
WIGYIYY	SWIRQPPGKGL	Salaayy	LSLTCTVS	LVKPSE	QESGP	QVQ	(1)	VH4-59
WIGYIYY	SWIRQPPGKGL	SSISSYY	LSLTCTVS	LVKPSE	QESGP	QVQ	(1)	Consensus
- Section 2								
106	90	30)		60	54	(54)	
GOWLVPD	ADTAVYYCARD:	LKLNSVT	VDTSKNOF	KSRUTŪ	YYNPS	EGN		A15-6.2 HC
	ADTAVYYCAR-	KT SSVT	VDTSKNOF	RSRUTT	RANA	яся	(54)	VH4-59
	ADTAVYYCAR		VDTSKNQF			SG		Consensus
- Section 3		DIE					(0.7)	
00000000				121		107	1071	
				vsvss	WGQGT	AFD		A15-6.2 HC
							(98)	VH4-59

positives: 77.7% identity: 75.2%

									Section 1
	(1)	1		3	20_	30		40	54
A15-6.2 LC	(1)	DIV	rospis	LPVIPG	EPASISC	ASSOSLA	Gangnny	LDWYLQ K	PGOSPOLLIS
A19	(1)	DIV	M Oab I, s	LEYTEG	EPASLUL	:Kaaoari	Hangyny	LDWYLOR	be@abdrrt?
Consensus	(1)	DIVM	ITQ3PL3	LPV PG	EPASISC	LIEDEERS	ang na	LDMATGK	PGQSPQLLIY
									Section 2
	(55)	55	60	70)	80	90		108
A15-6.2 LC	(55)	LGBI	RASGVE	DRFSGS	GSGTDF1	LKISAVE	ADDVGEY	YCMOALC	IPLTFGGGT
Ā19	(55)					TRIBRVE			
Consensus	(55)	real	IRASGVP	DRFSGS	GSGTDFT	LKISRVE	ADDVGIY	YCMQALC	P
									Section 3
1	(109)	109 1	12						
A15-6.2 LC	(109)	VEIF	-						
Ā19									
Consensus	(109)	•		positive	8 B5-7% d	entity, 83.9%			

							Section 1
	(1)	1			<u>.</u>	10	<u>40</u> 53
A15-6.9 HC	(1)	ÖVÖLE	QBGPGLVK	PSETLSLI	'CTVBGGST	BGTYHWSW.	TROHEGRGLEWIGY
VH4-31	(1)	QVQL	EBGEGLVK	ьзотгати	CTVŠGSSI	BSGGYYWSW	IRQHPGKGLEWIGYI
Consensus	à	QVQL	SGPGLVK	PS TLSLT	CTVSGGSI	SSG YHWSW	IRQHPGKGLEWIGYI
							Section 2
	(54)	54	60	70	80	90	108
A15-6.9 HC	(54)		mvander v	epilmi eni	mernorar.	z z e e nih X k ni	TAVYYCARGGDGYRY
VH4-31	(54)					KLSSVTAAD	
	. ,	Limited Street	Market Committee of the	Charles and the second second second	ACCOMMONDED TO THE STATE OF THE PARTY OF THE	of the could be found that the second to the second the	are the the tree is a contract that we are a contract to the c
Consensus	(34)	TIBGS	STAUNDSTR	SKITISVL	TSKNOFSLI	CLSSVTAAD	
							Section 3
. 4	(107)	107	117				
A15-6.9 HC	(107)	WGQGT	LVTVSS				
VH4-31	(100)						
Consensus	• •						
			hos	itives: 81,2%	identity: 77.8%		

FIGURE 33

								Section 1
	(1)	1	,10	2	0	30	,4 0	54
A15-6.9_LC	(1)	EIV	MTQSPATL	SVSPGERAT	LECRASOS	SNNFAWY	QQKPGQAP	RLLI F GASTR
12	(1)	EIV	MTQSPATL	SVSPGERAT	Lacrasoa	ISSNLAWY	QQKPGQAP	RLLIYGASTR
Consensus	(1)	EIV	MTQSPATL	SVSPGERAT	LSCRASQSI	YWA N BI	'QQKPGQAP	RLLIFGASTR
								Section 2
	(55)		.60	70	80	. 9		107
A15-6.9_LC	(55)	ATG	IPARF 868	GSGTEFTLI	'ISSLQSEDI	PAVYYCQC	YNNWPRTF	GQGTKVEIK
1.2	(55)	ATG	IPARF968	GSGTEFTLT	'ISSLQSEDI	PAVYYCOĆ	YNNWP	
Consensus	(55)	ATG	IPARF SG S	GSGTEFTLT	ISSLQSED!	PAVYYCQQ	YNNWP	

positives: 86.9% | identity: 85.0%

	(4)	1	10		20	30	40	—— Section 1 53
445 6 44 110	(1)	(September 1						
A15-6.11 HC	(1)						YHWSWIROHP	
VH4-31	(1)						EAKAMBMI BOHE	
Consensus	(1)	QVQL	QESGPG	LVKPSQTL	SLTCTV	78GGSISSG	YHWSWIRQHP	GKGLEWIGYI
								Section 2
	(54)	54	60	70		80	90	106
445.6.44 110				nesa Surcent Lorden in	NAC SAME OF STREET	www.maranananananananananananananananananana	A PROCESS OF THE PROPERTY OF THE	CONTRACT.
A15-h 11 HC	1541	MY SC	STYVND	SIKSRVTI	SUDTER	NOFSKIR	YYVXATITAATUF	PARGGDGYKY
	(54) (54)	YYSG	STYYNP	SLKSRVII atkanumt	BVDTBF	NOFSLKLS	YYVATDAATÜE VVVIATORATVV	ZARGGDGYKY ZARGGDGYKY
A15-6.11_HC VH4-31	(54)	AAac	STYYNP	SLKSRVTI	SVDTSE	MOFSLKLS	YYVATDAATVE	CAR
	(54)	AAac	STYYNP	SLKSRVTI	SVDTSE	MOFSLKLS	YYVATDAATVE YYVATDAATVE YYVATDAATVE	CAR
VH4-31 Consensus	(54) (54)	AA8e	STYYNP STYYNP	SLKSRVTI SLKSRVTI	SVDTSE	MOFSLKLS	YYVATDAATVE	TAR
VH4-31 Consensus	(54)	AA8e	STYYNP	SLKSRVTI SLKSRVTI	SVDTSE	MOFSLKLS	YYVATDAATVE	CAR
VH4-31 Consensus	(54) (54) —— (107)	YY86 YY86	STYYNP STYYNP 11	slkskyti slkskyti 7	SVDTSE	MOFSLKLS	YYVATDAATVE	CAR
VH4-31 Consensus	(54) (54) (54) (107) (107)	YY86 YY86	STYYNP STYYNP 11	slkskyti slkskyti 7	SVDTSE	MOFSLKLS	YYVATDAATVE	CAR

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							Section 1
	(1)	1	.10	20	30	40	53
A15-6.11_LC	(1)	EIVMI	QSPATLS.	/SPGERATISCE	Tuneasdey	awyqqkpgqap	RLLIYGAST
2ا -	(1)	elvmi	CHEATER	Begeratisce	<u> Abosvasni</u>	AWYQQKPGQAP	RLLIÝGAST
Consensus	(1)	EIVMI	PATE STATES	SPGERATLSCF	IN SVSOSA	AWYQQKPGQAP	RLLIYGAST
							Section 2
	(54)	54	60	70	80	90	106
A15-6.11 LC	(54)		PARPSGEO	SECTRETITIES	LOSEDFAVY	YCOOYNNWPRT	FGQGTKVEI
12	(54)			.agreetLtia			
Consensus	(54)			SGTEFTLTISS			
							Section 3
	(107)	107	•				
A15-6.11 LC	·						
L2	(96)	_					
Consensus	٠,						
	,		positive	si 67.9% i lidentiry e	7.9%		

CLONE #	¥	#DEL	VH END	s,N#	N Sequence	占	Size of D	D Sequence	s,N#	N Sequence	3	# del	JH Segmen
A15-3.10	DP-71/4-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTF
A15-3.22	DP-65/4-31	0	GAGAGA	စ	GGGAGATGG			•			JH4B	4	CTTTGA
A15-3.27	DP-71/4-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTI
A15-3.45	DP-14/1-18	0	GAGAGA	6	AACTAA	03-10	12	GGTTCGGGGAGT	~	8	JH6B	6	ACTACT
A15-3.65	DP-65/4-31	0	GAGAGA	8	TCGGGAAA	D6-13	8	CAGCTGGT	4	E	JH5A	-11	GACTAC
A15-6.1	DP-49/3-30	6	GCGAGA	-	_	D3-3	18	CGATTTTTGGAGTGGTTA	က	106	JH6B	-12	ACTACG
A15-6.2	DP-71/4-59	0	GAGAGA	7	TCCAGGC	D6-19	11	CAGTGGCTGGT	5	CCCTG	ЭНЗВ	0	ATGCTT
A15-6.9	DP-65/4-31	_	CGAGAG	3	999	D5-24	11	GAGATGGCTAC	4	AGAT	H,	-16	ACTGGG
A15-6.11	DP-65/4-31	-	CGAGAG	e	999	D5-24	13	GAGATGGCTACAA	2	TS)H	-16	ACTGGG
A15-6.12	DP-65/4-31	-	CGAGAG	က	999	D5-24	11	GAGATGGCTAC	4	AGAT	JH1	-16	ACTGGG
CLONE	ķ	#del	vk end	ŧ	N SEQ	š	# del	JK end					
A15-3.10	02/012/DPK		CCCTCC	6	GGAGTGCAG	왕	2-	TTTGG					
A15-3.22	A30	က	TTACCC	0	0	ZK4	0	GCTCAC					
A15-3.27	A30	က	TTACCC	0	0	ξ.	0	GTGGAC					
A15-3.45	B3/DPK24	-	TCCCTC	က	GGT	JK1	9-	cerrce					
A15-3.65	08/018/DPK	-	TCCCTC	0	0	첫 왕	-2	TCACTITC					
A15-6.1	A20/DPK4	60	GTCCCC	0	0	JK3	0	ATTCAC					
A15-6.2	A3/A19/DPK	-	TTCCTC	0	0	JK4	-5	TCACTTTC					
A15-6.9	L2/DPK21	-	GGCCTC	0	0	JK1	-2	GGACGTT					
A15-6.11	L2/DPK21	_	GGCCTC	0	0	폿	-2	GGACGTT					
A15-6.12	12/DPK21	-	GGCCTC	°	0	-X	-2	GGACGTT					